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RAW SEQUENCE LISTING DATE: 03/12/2002

PATENT APPLICATION: US/09/873,829

TIME: 09:54:51

Input Set : N:\Crf3\RULE60\09873829.raw
Output Set: N:\CRF3\03122002\1873829.raw

SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
             (i) APPLICANT: Choi, Yongwon
                             Wong, Brian
      б
      7
                             Josien, Regis
      8
                             Steinman, Ralph
            (ii) TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
     10
     11
                                       INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING
SAME, AND
     12
                                      METHODS OF USE THEREOF
     14
           (iii) NUMBER OF SEQUENCES: 18
     16
            (iv) CORRESPONDENCE ADDRESS:
     17
                   (A) ADDRESSEE: Klauber & Jackson
     18
                   (B) SIREET: 411 Hackensack Avenue, 4th Floor
     19
                   (C) CITY: Hackensack
     20
                   (D) STATE: New Jersey
     21
                   (E) COUNTRY: USA
     2.2
                   (F) ZIP: 07601
     24
             (V) COMPUTER READABLE FORM:
     25
                  (A) MEDIUM TYPE: Floppy disk
                   (B) COMPUTER: IBM PC compatible
     26
     27
                   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     28
                   (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
     30
            (vi) CUERENT APPLICATION DATA:
C--> 31
                   (A) APPLICATION NUMBER: US/09/873,829
C--> 32
                   (B) FILING DATE: 04-Jun-2001
     33
                   (C) CLASSIFICATION:
     3.5
           (vii) PRIOR APPLICATION DATA:
                  (A) APPLICATION NUMBER: 09/210,115
     36
     37
                   (B) FILING DATE:
          (viii) ATTORNEY/AGENT INFORMATION:
     4()
     41
                   (A) NAME: Jackson Esq., David A.
     4.2
                   (B) REGISTRATION NUMBER: 26,742
                  (C) REFERENCE/DOCKET NUMBER: 600-1-200 CIP N
     43
            (ix) TELECOMMUNICATION INFORMATION:
     45
     46
                  (A) TELEPHONE: 201-487-5800
                  (B) TELEFAX: 201-343-1684
     47
     48
                  (C) TELEX: 133521
     51 (2) INFORMATION FOR SEQ ID NO: 1:
     53
             (i) SEQUENCE CHARACTERISTICS:
     54
                  (A) LENGTH: 1823 base pairs
     55
                  (B) TYPE: nucleic acid
     56
                  (C) STRANDEDNESS: double
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(D) TOPOLOGY: linear

57

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PATE: 03/12/2002

Input Set : N:\Crf3\RULE60\09873829.raw Output Set: N:\CRF3\03122002\1873829.raw

59 (ii) MOLECULE TYPE DDNA													
61 (iii) HYPOTHEIICAL: NO													
63 (vi) ORIGINAL SOURCE:													
64 (A) ORGANISM Homo sapiens													
(ix) FEATURE:													
6' (A) NAME/KEY. CDS													
(B) LOCATION: 1738													
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:													
73 CAG ATG GAT CCT AAT AGA ATA TCA GAA GAT GGC ACT CA	C TGC ATT TAT 48												
74 Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr Hi													
75 1 5 10 10	15												
77 AGA AII TIG AGA CIC CAI GAA AAI GCA GAI TII CAA GA													
78 Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln As													
79 20 25	30												
81 GAG AGI CAA GAT ACA AAA TTA ATA CCT GAT TCA IGT AG													
82 Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Ar													
	5												
85 CAG GCC TTI CAA GGA GCT GTG CAA AAG GAA TTA CAA CA													
86 Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln Hi													
87 50 55 60	3113 (41 31)												
8+ TCA CAG CAC ATC AGA GCA GAG AAA GCG ATG GTG GAT GG	C TCA TGG TTA 240												
90 Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gl													
91 65 70 75	80												
93 GAT CTG GCC AAG AGG AGC AAG CTT GAA GCT CAG CCT TT													
94 Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Ph													
95 85 90	95												
97 ACT ATT AAT GCC ACC GAC ATC CCA TCT GGT TCC CAT AA													
98 Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Ly													
99 100 105	110												
101 TCC TCT TGG TAC CAT GAT CGG GGG TGG GGT AAG ATC T													
102 Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile S													
	25												
105 TIT AGC AAT GGA AAA CTA ATA GTT AAT CAG GAT GGC T	TT TAI TAC CTG 432												
106 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly P													
107 130 135 140													
109 TAT GCC AAC AIT TGC TTT CGA CAT CAT GAA ACT TCA G	GA GAC CTA GCT 480												
110 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser G	ly Asp Leu Ala												
111 145 150 155	160												
113 ACA GAG TAT CTT CAA CTA ATG GTG TAC GTC ACT AAA A	CC AGC ATC AAA 528												
114 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys T													
115 165 170	175												
117 ATC CCA AGT TCT CAT ACC CTG ATG AAA GGA GGA AGC A	CC AAG TAT TGG 576												
118 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser T													
119 180 185	190												
121 TCA GGG AAT TCT GAA TTC CAT TTT TAT TCC ATA AAC G													
122 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn V													
-	05												
125 TIT AAG TTA CGG TCT GGA GAG GAA ATC AGC ATC GAG G	TC TCC AAC CCC 672												
126 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu V													
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Input Set : N:\Crf3\RULE60\09873829.raw
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127	2	10					215					220						
	ICC I		TG	GAT	(7)7(7)	GAT		GAT	GCA	ACA	TAF		-3GG	аст	TTT	AAA		720
	Ser L																	2 0
	225			. тор		230	3111				235		31 !			240		
	GII C	GA :	JAT	ATA	GAT		GCC	CCAG	TTT	TIGG		TT A	IGTA	TIIC	C			768
	Val A																	
135		- , .			245													
	IGGAI	GIT	rg o	GAAAG		TT T	TAAA	ACAA(g idd.	AAGA	AAGA	TGI	ATAT	AGG	TGTG	TGAG.	AC	828
	TACTA																	888
	AACAC																	948
	ITAAA																	1008
145	AIGAG	AAA	CT (GCATO	G TiGiGi	GC TA	A TIGIGI	GAGG	G GT	TGGT	CCCT	GGT	CATG	IGC	CCCT	rege.	AG	1068
	CIGAA																	1128
149	TTGAA	TTGI	T A	CATO	CATG	CT G	GAAC	CIGCA	AA A	AAAT	ACTT	ГΤΓι	C'FAA'	TGA	GGAG	AGAA.	AA	1188
15.1	TATAT	GTAI	T I	TTAT	TATA	AT A	ICTA	AAGT	T AT	ATTT	CAGA	IGT	AATG	ΤΤΤ	TCTT	TGCA.	AA	1248
153	GTATT	GTAA	AA 1	TAT	ATTTO	GT G	CTATA	AGTA	TT	GATT	CAAA	ATA	TTTA	AAA	ATGT	CITG	CT	1308
155	GTTGA	CATA	T T	[AA]	IGTT.	IT A	AA [G]	TACA	G AC	ATAT	TTAA	CIG	GTGC	ACT	TIGIA	TAAA	TC	1368
157	CCTGG	GGAA	AA A	ACTTO	GCAG	CT A	4GGA(3GGG <i>A</i>	AA.	AAAT	GTTG	TTT	CCTA	ATA	TCAA	ATGC	AG	1428
159	TATAT	TTCI	TT C	GITC	CTTT	ГТ Ал	AGTTA	AATA	G AT	ГТТТ	TCAG	ACT	rgrez	AAG	CCTG	rgca.	AA	1488
161	AAAAT	TAAA	AA I	[GGA]	race:	IT G	AATAA	ATAA	G CA	GGAT(GTTG	GCC	ACCA	GGT	GCCT	TCA	AA	1548
163	IITAG	AAAd	CT A	AATTO	GACT.	IT A	GAAA	GCTGA	A CA	FIGC	CAAA	AAG	GATA	CAT	AATG	GGCC	AC	1608
165	IGAAA	TCTO	GT (CAAGA	AGTAC	GT TA	ATATA	TTA	G TT	GAAC	AGGT	GTT	TTTC	CAC	AAGT(GCCG	CA	1668
167	AATTG	TACC	CT T	LLLL	TGT	TT T	TTTC	AAAA	r AG	AAAA	GTTA	TTA	GTGG	TTT	ATCA	GCAA	AA	1728
	AAGTC										TGTA	CAA	ΓΑΑΑ	AAC	ATTG	CCTT	ΙG	1788
171	887777																	
				TTTC						CGC								1823
174	(2) I	NFOF	RMAT	NOI	FOR	SEQ	ID I	: OF	2:	CGC								1823
174 176	(2) I	NFOF	RMAT SEÇ	ION PUENC	FOR CE CE	SEQ HARA	ID I	NO: Z ISTIC	2: CS:									1823
174 176 177	(2) I	NFOF	RMAT SEQ (A	CION QUENC A) LE	FOR CE CE ENGTE	SEQ HARA(H: 24	ID 1 CTER: 45 ar	NO: Z ISTIC mino	2: CS:									1823
174 176 177 178	(2) I	NFOF	RMAT SEÇ (<i>A</i>	TION QUENC A) LE B) TY	FOR CE CE ENGTE YPE:	SEQ HARA H: 24 amin	ID 1 CTER: 45 ar no ac	NO: Z ISTIC mino cid	2: CS:									1823
174 176 177 178 179	(2) I	NFOE	RMAT SEÇ (A (E	TION QUENÇ A) LE B) TY	FOR CE CH ENGTH ZPE: DPOLO	SEQ HARAG H: 29 amin DGY:	ID N CTER: 45 ar no ac line	NO: Z ISTIC mino cid ear	2: CS:									1823
174 176 177 178 179 181	(2) I	NFOF	RMAT SEÇ (A (E (E MOI	TION QUENCA) LE B) TY C) TO LECUI	FOR CE CH ENGTH (PE: OPOLO LE TY	SEQ HARAGH: 20 amin DGY: YPE:	ID 1 CTER: 45 ar no ac line prot	NO: Z ISTIC mino cid ear tein	2: CS: acid	ds								1823
174 176 177 178 179 181 183	(2) I	NFOF (i) ii) xi)	RMAT SEQ (A (E (E MOI SEQ	TION QUENCA) LE B) TY D) TO QUENC	FOR CE CH ENGTH (PE: DPOLO LE TY CE DE	SEQ HARA(H: 24 amin DGY: YPE: ESCE:	ID NOTER: 45 are no according protections IPTIC	NO: A ISTIC mino cid ear tein ON: S	2: CS: acid	is ID N (II.	Cua	Tlo	Tue		1823
174 176 177 178 179 181 183 185	(2) I (((Gln M	NFOF (i) ii) xi)	RMAT SEQ (A (E (E MOI SEQ	TION QUENCA) LE B) TY D) TO QUENC	FOR CE CE CENGTE CPOLO DPOLO LE TY CE DE ASN	SEQ HARA(H: 24 amin DGY: YPE: ESCE:	ID NOTER: 45 are no according protections IPTIC	NO: A ISTIC mino cid ear tein ON: S	2: CS: acid	ds ID N Asp			His	Cys		Tyr		1823
174 176 177 178 179 181 183 185	(2) I (() Gln M 1	NFOF (i) ii) xi) et A	RMAT SEÇ (A (E (D MOI SEÇ ASP	TION QUENCA) LH A) LH B) TO LECUI QUENC	FOR CE CH ENGTH (PE: DPOLO LE TY CE DE Asn 5	SEQ HARAGH: 28 amin DGY: YPE: ESCE: Arg	ID ! CTER. 45 and ad line prof IPTIC Ile	NO: A ISTIC mino cid ear tein DN: S	2: CS: acio SEQ: Glu	ds ID NO Asp 10	Gly	Thr			15			1823
174 176 177 178 179 181 183 185 186	(2) I (((Gln M	NFOF (i) ii) xi) et A	RMAT SEÇ (A (E (D MOI SEÇ ASP	TION QUENC A) LH B) TY .ECUI QUENC Pro Arg	FOR CE CH ENGTH (PE: DPOLO LE TY CE DE Asn 5	SEQ HARAGH: 28 amin DGY: YPE: ESCE: Arg	ID ! CTER. 45 and ad line prof IPTIC Ile	NO: A ISTIC mino cid ear tein DN: S	2: CS: acid SEQ: Glu Ala	ds ID NO Asp 10	Gly	Thr		Thr	15			1823
174 176 177 178 179 181 183 185 186 188	(2) I (4) (5) (6) Arg I	NFOH (i) ii) xi) et A	RMAT SEÇ (A (E (D MOI SEÇ Asp	TION QUENCA) LH B) TY LECUI LECUI QUENC Pro Arg 20	FOR CE CE ENGTH ZPE: DPOLO LE TY CE DE Asn 5 Leu	SEQ HARAGH: 20 amin DGY: YPE: ESCE: Arg	ID 1 CTER: 45 am no ac line prot IPTIC Ile	NO: A ISTIC mino cid ear tein ON: S Ser	2: CS: acid SEQ: Glu Ala 25	ds ID No Asp 10 Asp	Gly Phe	Thr Gln	Asp	Thr	15 Thr	Leu		1823
174 176 177 178 179 181 183 185 186 188	(2) I (() Gln M 1	NFOH (i) ii) xi) et A	RMAT SEÇ (A (E MOI SEÇ Asp Leu	TION QUENCA) LH B) TY LECUI LECUI QUENC Pro Arg 20	FOR CE CE ENGTH ZPE: DPOLO LE TY CE DE Asn 5 Leu	SEQ HARAGH: 20 amin DGY: YPE: ESCE: Arg	ID 1 CTER: 45 am no ac line prot IPTIC Ile	NO: A ISTIC mino cid ear tein ON: S Ser Asn	2: CS: acid SEQ: Glu Ala 25	ds ID No Asp 10 Asp	Gly Phe	Thr Gln	Asp Arg	Thr	15 Thr	Leu		1823
174 176 177 178 179 181 183 185 186 188 189 191	(2) I ((Gln M	NFOF (i) ii) xi) et A	RMAT SEÇ (A (E MOI SEÇ Asp Leu	TION QUENCA) LE B) TY LECUI QUENC Pro Arg 20 Asp	FOR CE CHENGTH (PE: DPOLCE TY Asn 5 Leu	SEQ HARAGH: 28 amin DGY: YPE: YPE: Arg His	ID NOTER. 45 are no accomposed protection. IPTIC Ile Glu Leu	NO: A ISTIC mino cid ear tein ON: S Ser Asn Ile 40	ES: acid SEQ: Glu Ala 25 Pro	ds ID No Asp 10 Asp Asp	Gly Phe Ser	Thr Gln Cys	Asp Arg 45	Thr 30 Arg	15 Thr Ile	Leu Lys		1823
174 176 177 178 179 181 183 185 186 188 189 191 192	(2) I (Gln M 1 Arg I Glu S Gln A	NFOF (i) ii) xi) et A le I	RMAT SEC (E (E MOI SEC Asp Leu 35	TION PUENCA) LE B) TO D) TO DECUI PUENC Pro Arg 20 Asp	FOR CE CHENGTH (PE: DPOLO LE TY Asn 5 Leu Thr	SEQ HARACH: 20 amin DGY: YPE: ESCE: Arg His Lys	ID 1 CTER. 45 ar no ad line prot IPTIC Ile Glu Leu Val	NO: Asn ISTIC mino cid ear tein ON: S Ser Asn Ile 40 Gln	2: acid SEQ : Glu Ala 25 Pro	ds ID NO Asp 10 Asp Asp Glu	Gly Phe Ser Leu	Thr Gln Cys Gln	Asp Arg 45 His	Thr 30 Arg	15 Thr Ile Val	Leu Lys		1823
174 176 177 178 179 181 183 185 186 188 189 191 192 194 195	(2) I ((Gln M 1 Arg I Glu S Gln A	NFOH (i) ii) xi) et A le I er G	RMAT SEQ (A (E (E MOI SEQ Asp Leu 35	TION PUENCA) LE B) TY D) TO LECUI PUENC Pro Arg 20 Asp	FOR CE CE CENGTE (PE: DPOLO LE TY Asn 5 Leu Thr	SEQ HARAGH: 26 amin DGY: YPE: ESCH: Arg His Lys	ID 1 CTER: 45 ar no ac line prot IPTIC Ile Glu Leu Val	NO: Asn Ile ASn Ile Gln	2: CS: acid SEQ: Glu Ala 25 Pro	ds ID No Asp 10 Asp Asp Asp	Gly Phe Ser Leu	Thr Gln Cys Gln 60	Asp Arg 45 His	Thr 30 Arg	15 Thr Ile Val	Leu Lys Gly		1823
174 176 177 178 179 181 183 185 186 188 191 192 194 195	(2) I ((Gln M 1 Arg I Glu S Gln A Ser G	NFOH (i) ii) xi) et A le I er G	RMAT SEQ (A (E (E MOI SEQ Asp Leu 35	TION PUENCA) LE B) TY D) TO LECUI PUENC Pro Arg 20 Asp	FOR CE CE CENGTE (PE: DPOLO LE TY Asn 5 Leu Thr	SEQ HARACHE 20 amin DGY: YPE: ESCRI Arg His Lys Ala	ID 1 CTER: 45 ar no ac line prot IPTIC Ile Glu Leu Val	NO: Asn Ile ASn Ile Gln	2: CS: acid SEQ: Glu Ala 25 Pro	ds ID No Asp 10 Asp Asp Asp	Gly Phe Ser Leu	Thr Gln Cys Gln 60	Asp Arg 45 His	Thr 30 Arg	15 Thr Ile Val	Leu Lys Gly		1823
174 176 177 178 179 181 183 185 186 188 191 192 194 195 197	(2) I (1) (2) (3) (4) (5) (6) (7) (7) (7) (7) (7) (7) (7) (7) (7) (7	NFOR (ii) iii) ext A er C lla F 50 lln F	RMAT SEÇ (A (E (I MOI SEÇ Asp Leu 35	TION DUENCA) LE B) TY D) TC LECUI DUENC Pro Arg 20 Asp Gln Ile	FOR CE CR CPE: OPOLO LE TY ASN 5 Leu Thr Gly	SEQ HARAC H: 20 amin DGY: YPE: ESCE: Arg His Lys Ala Ala 70	ID 1 CTER. 45 ar no ac line prot IPTIC Ile Glu Leu Val 55 Glu	NO: ASINO GIN Lys	2: CS: acid SEQ: Glu Ala 25 Pro Lys	ID NO Asp 10 Asp Asp Glu Met	Gly Phe Ser Leu Val 75	Thr Gln Cys Gln 60 Asp	Asp Arg 45 His	Thr 30 Arg Ile Ser	15 Thr Ile Val	Leu Lys Gly Leu 80		1823
174 176 177 178 179 181 183 185 186 188 191 192 194 195 197	(2) I ((Gln M 1 Arg I Glu S Gln A Ser G	NFOR (ii) iii) ext A er C lla F 50 lln F	RMAT SEÇ (A (E (I MOI SEÇ Asp Leu 35	TION DUENCA) LE B) TY D) TC LECUI DUENC Pro Arg 20 Asp Gln Ile	FOR CE CR CPE: OPOLO LE TY ASN 5 Leu Thr Gly	SEQ HARAC H: 20 amin DGY: YPE: ESCE: Arg His Lys Ala Ala 70	ID METER. 45 ar no ac line profile IPTIC ILE Glu Leu Val 556	NO: ASINO GIN Lys	2: CS: acid SEQ: Glu Ala 25 Pro Lys	ID NO Asp 10 Asp Asp Glu Met	Gly Phe Ser Leu Val 75	Thr Gln Cys Gln 60 Asp	Asp Arg 45 His	Thr 30 Arg Ile Ser	15 Thr Ile Val	Leu Lys Gly Leu 80		1823
174 176 177 178 179 181 183 185 186 188 191 192 194 195 197 198 200 201	(2) I (1) (2) (3) (4) (5) (6) (7) (7) (7) (7) (7) (7) (7) (7) (7) (7	NFOR (ii) iii) et F er G la F 50 ln F	RMAT SEC (A (E (E MOI SEC Asp Leu Casp Dhe	TION DUENCA) LE B) TY B) TO LECUI DUENC PRO Arg 20 Asp Gln Ile Lys	FOR CE CHENGTH CPE: DPOLO LE TY DE DH Asn 5 Leu Thr Gly Arg 85	SEQ HARACHER 20 amin DGY: YPE: YPE: Arg His Lys Ala 70 Ser	ID to STER. 45 are no accline protocol IPTIC Ile Glu Leu Val 55 Glu Lys	NO: ASINO GIN Lys	ES: acio SEQ: Glu Ala 25 Pro Lys Ala Glu	ID NO Asp 10 Asp Glu Met Ala 90	Gly Phe Ser Leu Val 75 Gln	Thr Gln Cys Gln 60 Asp Pro	Asp Arg 45 His Gly Phe	Thr 30 Arg Ile Ser	15 Thr Ile Val Trp His 95	Leu Lys Gly Leu 80 Leu		1823
174 176 177 178 179 181 183 185 186 188 191 192 194 195 197 198 200 201	(2) I (Gin M 1 Arg I Glu S Gln A Ser G 65 Asp L	NFOR (ii) iii) et F er G la F 50 ln F	RMAT SEC (A (E (E MOI SEC ASP Leu Gln 35 Phe Lis Ala	TION DUENCA) LE B) TY B) TO LECUI DUENC PRO Arg 20 Asp Gln Ile Lys	FOR CE CHENGTH CPE: DPOLO LE TY DE DH Asn 5 Leu Thr Gly Arg 85	SEQ HARACHER 20 amin DGY: YPE: YPE: Arg His Lys Ala 70 Ser	ID to STER. 45 are no accline protocol IPTIC Ile Glu Leu Val 55 Glu Lys	NO: ASINO GIN Lys	ES: acio SEQ: Glu Ala 25 Pro Lys Ala Glu	ID NO Asp 10 Asp Glu Met Ala 90	Gly Phe Ser Leu Val 75 Gln	Thr Gln Cys Gln 60 Asp Pro	Asp Arg 45 His Gly Phe	Thr 30 Arg Ile Ser	15 Thr Ile Val Trp His 95 Ser	Leu Lys Gly Leu 80 Leu		1823
174 176 177 178 179 181 183 185 186 188 191 192 194 197 200 201 203 204	(2) I (Gin M 1 Arg I Glu S Gln A Ser G 65 Asp L	NFOR (ii) iii) et F er G la F 50 ln F	RMAT SEC (A (E (E MOI SEC ASP Leu 35 Phe His	TION DUENCA) LE B) TY C) TC LECUI DUENC Pro Arg 20 Asp Gln Ile Lys Ala 100	FOR CE CHENGTH CPE: DPOLOLE TY CE DE Asn 5 Leu Thr Gly Arg 85 Thr	SEQ HARACHER CONTROL HENDER CONTROL MARCHER CONTROL HIS Lys Ala Ala 70 Ser Asp	ID to CTER. 45 are no accline protocol IPTIC ILE Glu Leu Val 555 Glu Lys Ile	NO: ASINO GIN Lys	ES: acid SEQ: Glu Ala 25 Pro Lys Ala Glu Ser 105	ID NO Asp 10 Asp Glu Met Ala 90 Gly	Phe Ser Leu Val 75 Gln Ser	Thr Gln Cys Gln 60 Asp Pro His	Asp Arg 45 His Gly Phe Lys	Thr 30 Arg Ile Ser Ala Val 110	15 Thr Ile Val Trp His 95 Ser	Leu Lys Gly Leu 80 Leu		1823
174 176 177 178 179 181 183 185 186 189 191 194 194 200 201 203 204 206 207	(2) I (Gln M 1 Arg I Glu S Gln A Ser G 65 Asp L Thr I	NFOR (i) ii) ii) et F er G la F 50 ln F eu A er I 1	RMAT SEC (A (E (E MOI SEC Asp Leu Bln 35 Phe His	TION QUENCA) LE B) TY C) TC LECUI QUENC Pro Arg 20 Asp Gln Ile Lys Ala 100 Tyr	FOR CE CHENGTH (PE: DPOLOLE TY EE DH Asn 5 Leu Thr Gly Arg Arg His	SEQ HARACHER SECTION OF THE SECTION	ID to CIER. 45 are no accline protection. IPTIC ILE Glu Leu Val 555 Glu Lys Ile Arg	NO: ASINO GIN Lys Leu Pro Gly 120	Es: acid SEQ: Glu Ala 25 Pro Lys Ala Glu Ser 105 Trp	ds ID No Asp 10 Asp Glu Met Ala 90 Gly Gly	Gly Phe Ser Leu Val 75 Gln Ser Lys	Thr Gln Cys Gln 60 Asp Pro His	Asp Arg 45 His Gly Phe Lys Ser 125	Thr 30 Arg Ile Ser Ala Val 110 Asn	15 Thr Ile Val Trp His 95 Ser Met	Leu Lys Gly Leu 80 Leu Leu		1823

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,829 IIME: 09:54:52

DAIE: 03/12/2002

Input Set : N:\Crf3\RULE60\09873829.raw
Output Set: N:\CRF3\03122002\1873829.raw

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215 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys 216 216 165 170			-		ASII	rre	_		-	піз	піѕ	GIU			GIŽ	ush	Leu		
216					Trre	Lou				Val	Tur	Val			Thr	Cor	т 1 о		
214 11e Pro Ser Ser His Thr Leu Met Lys Gly Ser Thr Lys Tyr Trp 11+ 180 185 190 185 190 205 205 205 202 195 200 205 205 202 205 202 205 202 205 202 205 202 205 202 205 202 205 202 205 202 205 205 202 205			1111	GIU	1 1 1	Leu		гел	Met	val	171		1111	LyS	1111	ser		LyS	
180			ı l o	Dro	car	car		The	Lau	Mot	1		610	Cor	The	Lirc		Trn	
221 Ser Gly Ash Ser Glu Phe His Phe Tyr Ser Ile Ash Val Gly Gly Phe 222			116	PIO	Set		nis	1 111	Legu	Met	_	эту	Gry	ser	1111	_	1,1	пр	
195 200 205 205 206 207			cor	210	λαn		210	Dha	Uic	Dho		cor	Tlo	Acn	U = 1		21	Dho	
224 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro			261	GIY		261	Gru	E 1157	:113		1 1 1	261	116	NSII		GIY	Эту	rne	
229			Dho	I ve		λησ	Sar	alv	(2.1 m		τlρ	Sar	tla	Glu		Sor	Δen	Pro	
227 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys 228 225 230 235 240 240 245 240 245 240 245 245 240 245			THE	-	ьси	ara	JUL	OI.		GIU	110	Jei	110		VUI	JCI	A S II	110	
228 225 236 235 240 245 240 230 241 245			Ser		I en	Asn	Pro	Asn		Asn	Δla	Thr	Tvr		Glv	Ala	Phe	Lvs	
230				LCu	1. C. CI	asp.	110	-	.5111	шэр	n L u	1111	_	THE	211	i i i u	Tite	_	
231				Ara	Asp	Tle	Asp	20,					200						
233 (2) INFORMATION FOR SEQ ID NO: 3: 235			, , , ,	9			_												
235			(2)	INF	ORMA:	LION		SEO	ID I	: OV	3 :								
236																			
237 (B) TYPE: nucleic acid 238 (C) STRANDEDNESS: double 239 (D) TOPOLOGY: linear 241 (ii) MOLECULE TYPE: cDNA 243 (iii) HYPOTHETICAL: NO 245 (vi) ORIGINAL SOURCE: 246 (A) OFGANISM: Mus musculus 248 (ix) FEATURE: 249 (A) NAME/KEY: CDS 250 (B) LOCATION: 1421092 253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: 255 CCCACGICCC GGGGGGGGGGGGGGGGGGGGGGGGGGGG					,							îs.							
139					•	,					•								
241		238			, (¢	2) S	TRANI	DEDNI	ESS:	doub	ole								
143		239			(I	ο) Γ	POL	OGY:	line	ear									
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249		246			(A	(<i>F</i>	RGAN	ISM:	Mus	muso	culus	5							
250				(ix) FEA	A LU B I	Ε:												
253 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: 255 CCCACGICCC GGGGGAGCCAC IGCCAGGACC TITGIGAACC GGICGGGGCG GGGGCCGIGG 60 257 CGGAGTCTGC TCGGCGGTGG GTGGCCCGAG AAGGGAGAA ACGAICGCGG AGCAGGGCGC 120 259 CCGAACTCCG GGCGCCGCGC C AIG CGC CGG GCC AGC CGA GAC IAC GGC AAG 171 260 Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys W> 261 250 255 263 TAC CIG CGC AGC TCG GAA GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC 219 264 Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro Gly Val Pro His W> 265 260 265 270 267 GAA GGT CCG CIG CAC CCC GGG CCT TCT GCA CCG GCT CCG GCG CCA 267 268 Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro W> 269 275 280 285 271 CCC GCC GCC TCC CGC TCC AIG ITC CTG GCC CTC CTG GGG CTG GGA CTG 315 272 Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu W> 273 290 295 300					()	A) NA	AME/I	KEY:	CDS										
### 155 CCCACGICCC GGGGAGCCAC TGCCAGGACC TTTGTGAACC GGTCGGGGGG GGGGCCGTGG 60 ### 157 CGGAGTCTGC TCGGCGGTGG GTGGCCCGAG AAGGGAGAA ACGATCGCGG AGCAGGGCGC 120 ### 158 CCCACGICCC GGCGCGCGC C ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG 171 ### 159 CCGAACTCCG GGCGCCGCGC C ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG 171 ### 159 CCGAACTCCG GGCGCCGCGC C ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG 171 ### 159 CCGAACTCCG GGCACCCC CATG CGC AGC CGC AGC CCC AGC AAG 171 ### 159 CCGAACTCCG GGCAAC CCC GCG CCT TCT GCA CCC GGC GTC CCA CAC 219 ### 150 CCC GCC GCC CTG CAC CCC GCG CCT TCT GCA CCC GCT CCG GCG CCC ACC ACC ACC ACC ACC CCC ACC A																			
157 CGGGAGTCTGC TCGGCGGTGG GTGGCCCGAG AAGGGAGAGA ACGATCGCGG AGCAGGGCGC 120					,	-					_								
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W> 261 250 255 263 TAC CTG CGC AGC TCG GAA GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC 219 264 Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro Gly Val Pro His 267 W> 265 270 267 GAA GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT CCG GCG CCA 267 268 Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro W> 269 275 280 285 271 CCC GCC GCC TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG 315 272 Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu 4 W> 273 290 295 300			CCGA	AACTO	JCG () ۋا (راۋاۋ	JUGU(30 U											1/1
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267 GAA GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA 267 268 Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro W> 269 275 280 285 271 CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG 315 272 Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu W> 273 290 290 295 300	W>		I y I	Pen	Arg		361	914	JIU	Mec	-	261	эту	FIU	ЭГУ		FIO	1113	
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W> 269																			207
271 CCC GCC GCC CGC TCC CGC TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG 272 Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu Gly Leu Gly Leu W> 273 290 295 300	W>																		
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275 GGC CAG GTC TGC AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG 363		275	GGC	CAG	GTG	GTC	TGC	AGC	ATC	GCT	CTG	TTC	CTG	TAC	TTT	CGA	GCG	CAG	363
276 Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln																			
W> 277 305 310 315 320	W>													_		-			
279 ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC TGC TIT TAT AGA 411		279	ATG	GAT	CCT	AAC	AGA	ATA	TCA	GAA	GAC	AGC	ACT	CAC	TGC	TTT	TAT	AGA	411
280 Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg		280	Met	Asp	Pro	Asn	Arg	Ile	Ser	Glu	Asp	Ser	Thr	His	Cys	Phe	Tyr	Arg	
W> 281 325 330 335	M>	281					325					330					335		

RAW SEQUENCE LISTING

DATE: 03/12/2002 PATENT APPLICATION: US/09/873,829 TIME: 09:54:52

Input Set : N:\Crf3\RULE60\09873829.raw Output Set: N:\CRF3\03122002\1873829.raw

			CIG															459
	2 44	He	Leu	A r-⊒	Leu	His	Glu	Asn	Ala		Leu	Gln	Asp	Ser		Leu	Glu	
M>					3 4 0					345					350			
			GAA															507
		Ser	Sla		Ihr	Leu	Pro	Asp		Cys	Arg	Arg	Met	-	Gln	Ala	Phe	
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		Gln	Gly	Ala	Val	Gln	Lys		Leu	Gln	His	Ile		Gly	Pro	Gln	Arg	
M>			370					375					380					
			ΓCA															603
			Ser	Gly	Ala	Pro		Met	Met	Glu	Gly		Irp	Leu	Asp	Val		
M>							390					395					400	
			CGA															651
		Gln	Arg	Gly	Lys		Glu	Ala	Gln	Pro		Ala	His	Leu	Thr		Asn	
M>						405					410					415		5.61.0
			GCC															699
		Ala	Ala	Ser		Pro	Ser	GIY	ser		Lys	Val	Inr	Leu		ser	Trp	
M>					420					425					430			7.47
			CAC															747
		Tyr	His	_	Arg	GIY	rrp	Ala		He	Ser	Asn	мет		Leu	ser	ASN	
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			Glu															
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	331	CGA	GCT	GGT	GAA	GAA	ATT	AGC	ATT	CAG	GTG	TCC	AAC	CCT	TCC	CTG	CTG	1035
			Ala															
W>			530	•				535					540					
	335	GAT	CCG	GAT	CAA	GAT	GCG	ACG	TAC	TTT	GGG	GCT	TTC	AAA	GTT	CAG	GAC	1083
	336	Asp	Pro	Asp	Gln	Asp	Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Gln	Asp	
W>	337	545					550					555					560	
	339	ATA	GAC	TGA	GACI	CATI	TTC (STGGA	ACA1	T AC	CATO	GATO	G TCC	CTAGA	ATGT			1132
		He		*														
	343	TTGG	GAAAG	CTT	CTTAA	AAAA	AT GC	GATGA	ATGTO	CAT	CACAT	rgrg	TAAG	SACTA	ACT F	AGAC	GACATG	1192
	345	GCCC	CACGO	GTG I	TATGA	AAACI	IC AC	CAGCC	CCTCI	CTC	CTTGA	AGCC	CTGT	CACAC	GT 1	GTGI	TATATG	1252
	347	TAAA	AGTCC	CAT	AGGTO	GATG1	TT AC	SATTO	CATGO	G TGA	ATTAC	CACA	ACG0	STITI	TAC A	TTA	TTGTAA	1312
																	CTTACA	1372
	351	CGTC	GAGCI	TAT (GAAC	GGGGC	GT CA	CAGI	CTCI	GGI	CTAA	ACCC	CTGG	SACA1	GT C	CCAC	CTGAGA	1432

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/873,829

DATE: 03/12/2002 TIME 09 54:53

Input Set : N:\Crf3\RULE60\09873829.raw
Dutput Set N:\CRF3\03122002\1873829.raw

1.31 M:220 C Keyword misspelled or invalid format, [(A) APPLICATION NUMBER: 1 32 M: 220 C Keyword misspelled or invalid format. [(B) FILING DATE:] L 261 M 336 W. Invalid Amino Acid Number in Coding Region, SEQ ID:3 L.265 M:336 W. Invalid Amino Acid Number in Coding Region, SEQ ID:3 L.269 M-336 W. Invalid Amino Acid Number in Coding Fegion, SEQ ID:3 $\pm \cdot 273$ M.336 W. Invalid Amino Acid Number in Coding Fegion, SEQ ID:3 1.277 M 336 W Invalid Amino Acid Number in Coding Region, SEQ ID:3 L 281 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L.285 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L.289 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:293 M:336 W. Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:297 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:301 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:305 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:309 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:313 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:317 M.336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:321 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID.3 L:325 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:329 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:333 M:336 W: Invalid Amino Acid Number in Coding Fegion, SEQ ID:3 L:337 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3